

Contents

No. 1-2 1-330 issued May 1992
No. 3 331-492 issued June 1992

Armour SL → Harms CT 427

Bachellier S → Werts C 372

Bai X → Chen L 311

Baird E, Cooper-Bland S, Waugh R, DeMaine M, Powell W: Molecular characterisation of inter- and intra-specific somatic hybrids of potato using randomly amplified polymorphic DNA (RAPID) markers 469

Bancroft I, Bhatt AM, Sjodin C, Scofield S, Jones JDG, Dean C: Development of an efficient two-element transposon tagging system in *Arabidopsis thaliana* 449

Bandlow W → Schricker R 363

Beaumont C → McHale MT 337

Beier D, Beier H: Expression of variant nuclear *Arabidopsis* tRNA^{Ser} genes and pre-tRNA maturation differ in HeLa, yeast and wheat germ extracts 201

Beier H → Beier D 201

Bertin P, Lejeune P, Colson C, Canchin A: Mutations in *bgfY*, the structural gene for the DNA-binding protein H1 of *Escherichia coli*, increase the expression of the kanamycin resistance gene carried by plasmid pGR71 184

Bhatt AM → Bancroft I 449

Bodeau JP, Walbot V: Regulated transcription of the maize *Bronze-2* promoter in electroporated protoplasts requires the *C1* and *R* gene products 379

Bridges BA: Mutagenesis after exposure of bacteria to ultraviolet light and delayed photoreversal 331

Bron S → Oskam L 462

Bruenn J → Finkler A 395

Budde E → Schmidt U 71

Campbell DA → Wong S 225

Canchin A → Bertin P 184

Chak K-F → Soong B-W 177

Charbit A → Werts C 372

Chen J → Leu J-Y 411

Chen L, Cui Y, Qin M, Wang Y, Bai X, Ma Q: Identification of a *nodD*-like gene in *Frankia* by direct complementation of a *Rhizobium nodD*-mutant 311

Chen XJ, Wésolowski-Louvel M, Fukuhara H: Glucose transport in the yeast *Kluyveromyces lactis*. II. Transcriptional regulation of the glucose transporter gene *RAG1* 97

Chérit P → Vitart V 193

Colson C → Bertin P 184

Cooper-Bland S → Baird E 469

Coppin E → Debuchy R 113

Corces VG → Smith PA 65

Crawford NM → LaBrie ST 169

Crumey V → Norris E 106

Cui Y → Chen L 311

Das S → Shen W-H 388

Dean C → Bancroft I 449

Debuchy R, Coppin E: The mating types of *Podospora anserina*: functional analysis and sequence of the fertilization domains 113

De Greve H → Renckens S 53

DeMaine M → Baird E 469

De Paepe R → Vitart V 193

DiMaio JJ → Harms CT 427

Dujardin G → Ekwall K 136

Eichel-Streiber C von, Laufenberg-Feldmann R, Sartingen S, Schulze J, Sauerborn M: Comparative sequence analysis of the *Clostridium difficile* toxins A and B 260

Eigel L, Koop H-U: Transfer of defined numbers of chloroplasts into albino protoplasts by subprotoplast/protoplast microfusion: chloroplasts can be "cloned", by using suitable plastome combinations or selective pressure 479

Ekwall K, Kermorgant M, Dujardin G, Groudinsky O, Slonimski PP: The *NAM8* gene in *Saccharomyces cerevisiae* encodes a protein with putative RNA binding motifs and acts as a suppressor of mitochondrial splicing deficiencies when overexpressed 136

Ennis DG → Koch WH 443

Feldmann KA → LaBrie ST 169

Feng T-Y → Jacobs JD 302

Ferrero I → Wésolowski-Louvel M 89

Finkler A, Peery T, Tao J, Bruenn J, Koltin Y: Immunity and resistance to the KP6 toxin of *Ustilago maydis* 395

Flavell AJ, Smith DB: A *Ty1-copia* group retrotransposon sequence in a vertebrate 322

Friesenegger A → Wirth R 157

Fukuchi A → Hirochika H 209

Fukuhara H → Chen XJ 97

Fukuhara H → Wésolowski-Louvel M 89

Galli D → Weidlich G 161

Ganal MW → Martin GB 25

Gebhardt C → Leonards-Schippers C 278

Ghosh S, Lucchesi JC, Manning JE: The non-dosage compensated *LSP1-α* gene of *Drosophila melanogaster* lies immediately downstream of the dosage compensated *L12* gene 49

Gieffers W → Leonards-Schippers C 278

Gille H → Holz A 81

Goebel W → Hanke C 42

Goffrini P → Wésolowski-Louvel M 89

Gomada M, Inouye S, Imaishi H, Nakazawa A, Nakazawa T: Analysis of an upstream regulatory sequence required for activation of the regulatory gene *xylS* in xylene metabolism directed by the TOL plasmid of *Pseudomonas putida* 419

Gorishin IY → Kil YY 483

Gregg K → Vercoe PE 284

Groudinsky O → Ekwall K 136

Halboth S, Klein A: *Methanococcus voltae* harbors four gene clusters potentially encoding two [NiFe] and two [NiFeSe] hydrogenases, each of the cofactor F_{420} -reducing or F_{420} -non-reducing types 217

Hanke C, Hess J, Schumacher G, Goebel W: Processing by OmpT of fusion proteins carrying the HlyA transport signal during secretion by the *Escherichia coli* hemolysin transport system 42

Harada T, Ishikawa R, Niizeki M, Saito K: Pollen-derived rice calli that have large deletions in plastid DNA do not require protein synthesis in plastids for growth 145

Harms CT, Armour SL, DiMaio JJ, Middlestead LA, Murray D, Negrotto DV, Thompson-Taylor H, Weymann K, Montoya AL, Shillito RD, Jen GC: Herbicide resistance due to amplification of a mutant acetoxyhydroxyacid synthase gene 427

Hashimoto J, Hirabayashi T, Hayano Y, Hata S, Ohashi Y, Suzuka I, Utsgui T, Toh-EA, Kikuchi Y: Isolation and characterization of cDNA clones encoding *cde2* homologues from *Oryza sativa*: a functional homologue and cognate variants 10

Hata S → Hashimoto J 10

Hayano Y → Hashimoto J 10

Heim L → Lorentz A 436

Herder IF den, Rosell AMM, Zuilen CM van, Punt PJ, Hondel CAMJJ van den: Cloning and expression of a member of the *Aspergillus niger* gene family encoding α -galactosidase 404

Hernalsteens J-P → Renckens S 53

Hershey JW → Kang HA 487

Hess J → Hanke C 42

Hidaka M → Hidaka T 476

Hidaka M → Kobayashi T 355

Hidaka T, Hidaka M, Uozumi T, Seto H: Nucleotide sequence of a carboxyphosphonoenolpyruvate phosphonotomutase gene isolated from a bialaphos-producing organism, *Streptomyces hygroscopicus*, and its expression in *Streptomyces lividans* 476

Hildebrand M → Jacobs JD 302

Hillenga DJ → Oskam L 462

Hirabayashi T → Hashimoto J 10

Hirochika H, Fukuchi A, Kikuchi F: Retrotransposon families in rice 209

Hofnung M → Werts C 372

Hohn B → Shen W-H 388

Holz A, Schaefer C, Gille H, Jueterbock W-R, Messer W: Mutations in the *DnaA* binding sites of the replication origin of *Escherichia coli* 81

Hondel CAMJJ van den → Herder IF den 404

Horaud T → Wirth R 157

Höricker-Grandpierre C → Klein B 122

Horiuchi T → Kobayashi T 355

Imaishi H → Gomada M 419

Inouye S → Gomada M 419

Ishikawa R → Harada T 145

Jacobs JD, Ludwig JR, Hildebrand M, Kukel A, Feng T-Y, Ord RW, Volcani BE: Characterization of two circular plasmids from the marine diatom *Cylindrotheca fusiformis*: plasmids hybridize to chloroplast and nuclear DNA 302

Jen GC → Harms CT 427

Jones JDG → Bancroft I 449

José M → Raz R 252

Jueterbock W-R → Holz A 81

Kang HA, Schweißer HG, Hershey JWB: The two genes encoding protein synthesis initiation factor eIF-5A in *Saccharomyces cerevisiae* are members of a duplicated gene cluster 487

Kermorgant M → Ekwall K 136

Kessler B, Lorenzo V de, Timmis KN: A general system to integrate lacZ fusions into the chromosomes of gram-negative eubacteria: regulation of the *Pm* promoter of the *TOL* plasmid studied with all controlling elements in monocopy 293

Kikuchi F → Hirochika H 209

Kikuchi Y → Hashimoto J 10

Kil YV, Gorishin IY, Mironov VN, Kreneva RA, Perumov DA: Riboflavin operon of *Bacillus subtilis*: unusual symmetric arrangement of the regulatory region 483

Klein A → Halboth S 217

Klein B, Pawłowski K, Höricker-Grandpierre C, Schell J, Töpfel R: Isolation and characterization of a cDNA from *Cuphea lanceolata* encoding a β -ketoacyl-ACP reductase 122

Klipp W → Masepohl B 33

Kobayashi T, Hidaka M, Nishizawa M, Horiuchi T: Identification of a site required for DNA replication fork blocking activity in the rRNA gene cluster in *Saccharomyces cerevisiae* 355

Koch WH, Ennis DG, Levine AS, Woodgate R: *Escherichia coli* umuD mutants: DNA sequence alterations and UmuD cleavage 443

Koltin Y → Finkler A 395

Koop H-U → Eigel L 479

Kreneva RA → Kil YV 483

Kretzinger RH → Wong S 225

Kuhn J → Swift S 129

Kukel A → Jacobs JD 302

Kutsche M → Masepohl B 33

LaBrie ST, Wilkinson JQ, Tsay Y-F, Feldmann KA, Crawford NM: Identification of two tungstate-sensitive molybdenum cofactor mutants, chl2 and chl7, of *Arabidopsis thaliana* 169

Lai Y-K → Leu J-Y 411

Latch GCM → Murray FR 1

Laufenberg-Feldmann R → Eichel-Streiber C von 260

Lejeune P → Bertin P 184

Leonards-Schippers C, Gieffers W, Salamini F, Gebhardt C: The *R1* gene conferring race-specific resistance to *Phytophthora infestans* in potato is located on potato chromosome V 278

Leu J-Y, Sun YH, Lai Y-K, Chen J: A maize cryptic *Ac*-homologous sequence derived from an *Activator* transposable element does not transpose 411

Levine AS → Koch WH 443

Lorentz A, Heim L, Schmidt H: The switching gene *swi6* affects recombination and gene expression in the mating-type region of *Schizosaccharomyces pombe* 436

Lorenzo V de → Kessler B 293

Lu F-M → Soong B-W 177

Lucchesi JC → Ghosh S 49

Ludwig JR → Jacobs JD 302

Ma Q → Chen L 311

Magdolen V → Schricker R 363

Manning JE → Ghosh S 49

Martin GB, Ganal MW, Tanksley SD: Construction of a yeast artificial chromosome library of tomato and identification of cloned segments linked to two disease resistance loci 25

Martínez-Izquierdo JA → Raz R 252

Masepohl B, Kutsche M, Rieder K-U, Schmehl M, Klipp W, Pühler A: Functional analysis of the cysteine motifs in the ferredoxin-like protein FdxN of *Rhizobium meliloti* involved in symbiotic nitrogen fixation 33

Mathieu C → Vitart V 193

Matsabayashi T → Vera A 151

McHale MT, Roberts IN, Noble SM, Beaumont C, Whitehead MP, Seth D, Oliver RP: CIT-I: an LTR-retrotransposon in *Cladosporium fulvum*, a fungal pathogen of tomato 337

McKim KS, Starr I, Rose AM: Genetic and molecular analysis of the *dpy-14* region in *Caenorhabditis elegans* 241

Messer W → Holz A 81

Middlestadt LA → Harms CT 427

Mironov VN → Kil YV 483

Mochizuki N, Yamamoto M: Reduction in the intracellular cAMP level triggers initiation of sexual development in fission yeast 17

Montoya AL → Harms CT 427

Moya A → Raz R 252

Murray D → Harms CT 427

Murray FR, Latch GCM, Scott DB: Surrogate transformation of perennial ryegrass, *Lolium perenne*, using genetically modified *Acremonium endophyte* 1

Nakazawa A → Gomada M 419

Nakazawa T → Gomada M 419

Negrotto DV → Harms CT 427

Niizeki M → Harada T 145

Nishizawa M → Kobayashi T 355

Noble SM → McHale MT 337

Noguchi T, Takahashi H: Activation and quantitative estimation of bacteriophage T4 late regulatory signal in cis- and transconditon 319

Norris E, Sanders M, Crumety V, Tsubota SI: The identification of the *B⁸* breakpoint and of two possible *Bar* genes 106

Ohashi Y → Hashimoto J 10

Ohmae M → Yoshimoto H 327

Oliver RP → McHale MT 337

Ord RW → Jacobs JD 302

Oskam L, Hillenga DJ, Venema G, Bron S: The integrated state of the rolling-circle plasmid pTB913 in the composite *Bacillus* plasmid pTB19 462

Pawlowski K → Klein B 122

Peery T → Finkler A 395

Perumov DA → Kil YV 483

Powell W → Baird E 469

Pühler A → Masepohl B 33

Puigdomènech P → Raz R 252

Punt PJ → Herder IF den 404

Qin M → Chen L 311

Raz R, José M, Moya A, Martínez-Izquierdo JA, Puigdomènech P: Different mechanisms generating sequence variability are revealed in distinct regions of the hydroxyproline-rich glycoprotein gene from maize and related species 252

Renckens S, De Greve H, Van Montagu M, Hernalsteens J-P: *Petunia* plants escape from negative selection against a transgene by silencing the foreign DNA via methylation 53

Rieder K-U → Masepohl B 33

Roberts CF → Streatfield SJ 231

Roberts IN → McHale MT 337

Rose AM → McKim KS 241

Rosell AMM → Herder IF den 404

Saito K → Harada T 145

Salamini F → Leonards-Schippers C von 278

Sanders M → Norris E 106

Sartorius S → Eichel-Streiber C von 260

Sauerborn M → Eichel-Streiber C von 260

Schaefer C → Holz A 81

Schell J → Klein B 122

Schmehl M → Masepohl B 33

Schmidt H → Lorentz A 436

Schmidt U, Budde E, Stahl U: Self-splicing of a mitochondrial group I intron from the cytochrome *b* gene of the ascomycete *Podospora anserina* 71

Schmitz G, Theres K: Structural and functional analysis of the *Bz2* locus of *Zea mays*: characterization of overlapping transcripts 269

Schneider R, Schweiger M: The yeast RNA1 protein, necessary for RNA processing, is homologous to the human ribonuclease/angiogenin inhibitor (RAI) 315

Schricker R, Magdolen V, Bandlow W: A new member of the adenylate kinase family in yeast: *PAK3* is highly homologous to mammalian AK3 and is targeted to mitochondria 363

Schulte-Frohlinde D → Schünemann S 348

Schulze J → Eichel-Streiber C von 260
 Schumacher G → Hanke C 42
 Schünemann S, Schulte-Frohlinde D: Survival of phage M13 with uracils on one or both DNA strands 348
 Schweiger M → Schneider R 315
 Schwelberger HG → Kang HA 487
 Scofield S → Bancroft I 449
 Scott DB → Murray FR 1
 Seth D → McHale MT 337
 Seto H → Hidaka T 476
 Shen W-H, Das S, Hohn B: Mechanism of *Ds1* excision from the genome of maize streak virus 388
 Shillito RD → Harms CT 427
 Sjodin C → Bancroft I 449
 Slonimski PP → Ekwall K 136
 Smith DB → Flavell AJ 322
 Smith PA, Corces VG: The suppressor of hairy-wing binding region is required for gypsy mutagenesis 65
 Soong B-W, Lu F-M, Chak K-F: Characterization of the *cea* gene of the ColE7 plasmid 177
 Stahl U → Schmidt U 71
 Starr I → McKim KS 241
 Stewart SAB → Swift S 129
 Streatfield SJ, Toews S, Roberts CF: Functional analysis of the expression of the 3'-phosphoglycerate kinase *pgk* gene in *Aspergillus nidulans* 231
 Sugiura M → Vera A 151
 Sun YH → Leu J-Y 411
 Suzuka I → Hashimoto J 10
 Swift S, Kuhn J, Stewart SAB: Selection and analysis of non-interactive mutants in the *Escherichia coli* tryptophan synthase α subunit 129
 Takahashi H → Noguchi T 319
 Tanksley SD → Martin GB 25
 Tao J → Finkler A 395
 Theres K → Schmitz G 269
 Thompson-Taylor H → Harms CT 427
 Timmis KN → Kessler B 293
 Toews S → Streatfield SJ 231
 Toh-EA → Hashimoto J 10
 Töpfer R → Klein B 122
 Tsay Y-F → LaBrie ST 169
 Tsubota SI → Norris E 106
 Uozumi T → Hidaka T 476
 Utsgui T → Hashimoto J 10
 Van Montagu M → Renckens S 53
 Vedel F → Vitart V 193
 Venema G → Oskam L 462
 Vera A, Matsubayashi T, Sugiura M: Active transcription from a promoter positioned within the coding region of a divergently oriented gene: the tobacco chloroplast *rpl32* gene 151
 Vercue PE, Gregg K: DNA sequence and transcription of an endoglucanase gene from *Prevotella (Bacteroides) ruminicola* AR20 284
 Vitart V, De Paepe R, Mathieu C, Chétrit P, Vedel F: Amplification of substoichiometric recombinant mitochondrial DNA sequences in a nuclear, male sterile mutant regenerated from protoplast culture in *Nicotiana sylvestris* 193
 Volcani BE → Jacobs JD 302
 Walbot V → Bodeau JP 379
 Wang Y → Chen L 311
 Waugh R → Baird E 469
 Weidlich G, Wirth R, Galli D: Sex pheromone plasmid pAD1-encoded surface exclusion protein of *Enterococcus faecalis* 161
 Werts C, Charbit A, Bachellier S, Hofnung M: DNA sequence analysis of the *lamB* gene from *Klebsiella pneumoniae*: implications for the topology and the pore functions in maltoporin 372
 Wésolowski-Louvel M, Gofrini P, Ferrero I, Fukuhara H: Glucose transport in the yeast *Kluyveromyces lactis*. I. Properties of an inducible low-affinity glucose transporter gene 89
 Wésolowski-Louvel M → Chen XJ 97
 Weymann K → Harms CT 427
 Whitehead MP → McHale MT 337
 Wilkinson JQ → LaBrie ST 169
 Wirth R, Friesenegger A, Horaud T: Identification of new sex pheromone plasmids in *Enterococcus faecalis* 157
 Wirth R → Weidlich G 161
 Wong S, Kretzinger RH, Campbell DA: Identification of a new EF-hand superfamily member from *Trypanosoma brucei* 225
 Woodgate R → Koch WH 443
 Yamamoto M → Mochizuki N 17
 Yamashita I → Yoshimoto H 327
 Yoshimoto H, Ohmae M, Yamashita I: The *Saccharomyces cerevisiae* GAM2/SIN3 protein plays a role in both activation and repression of transcription 327
 Zuilen CM van → Herder IF den 404

Indexed in *Current Contents*